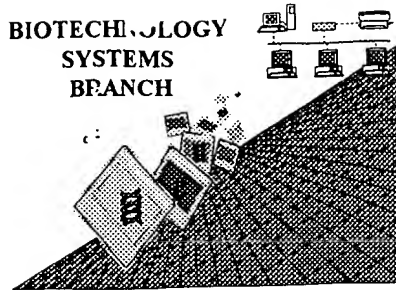


## **RAW SEQUENCE LISTING** **ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/842,745  
Source: OIP  
Date Processed by STIC: 5/11/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

**BEST AVAILABLE COPY**

OIPE

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/842,745

DATE: 05/11/2001  
 TIME: 10:44:47

Input Set : A:\2922-A.txt  
 Output Set: N:\CRF3\05112001\I842745.raw

Does Not Comply  
 Corrected Diskette Needed

P. 2

3 <110> APPLICANT: Fanslow III, William C.  
 4 Thomas, Elaine K.  
 6 <120> TITLE OF INVENTION: METHOD FOR TREATMENT OF TUMORS USING PHOTODYNAMIC  
 7 THERAPY  
 9 <130> FILE REFERENCE: 2922-A  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/842,745  
 C--> 12 <141> CURRENT FILING DATE: 2001-04-25  
 14 <160> NUMBER OF SEQ ID NOS: 3  
 16 <170> SOFTWARE: PatentIn Ver. 2.0  
 18 <210> SEQ ID NO: 1  
 19 <211> LENGTH: 260  
 20 <212> TYPE: PRT  
 21 <213> ORGANISM: Mus sp.  
 23 <400> SEQUENCE: 1  
 24 Met Ile Glu Thr Tyr Ser Gln Pro Ser Pro Arg Ser Val Ala Thr Gly  
 25 1 5 10 15  
 27 Leu Pro Ala Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu  
 28 20 25 30  
 30 Ile Thr Gln Met Ile Gly Ser Val Leu Phe Ala Val Tyr Leu His Arg  
 31 35 40 45  
 33 Arg Leu Asp Lys Val Glu Glu Glu Val Asn Leu His Glu Asp Phe Val  
 34 50 55 60  
 36 Phe Ile Lys Lys Leu Lys Arg Cys Asn Lys Gly Glu Gly Ser Leu Ser  
 37 65 70 75 80  
 39 Leu Leu Asn Cys Glu Glu Met Arg Arg Gln Phe Glu Asp Leu Val Lys  
 40 85 90 95  
 42 Asp Ile Thr Leu Asn Lys Glu Glu Lys Lys Glu Asn Ser Phe Glu Met  
 43 100 105 110  
 45 Gln Arg Gly Asp Glu Asp Pro Gln Ile Ala Ala His Val Val Ser Glu  
 46 115 120 125  
 48 Ala Asn Ser Asn Ala Ala Ser Val Leu Gln Trp Ala Lys Lys Gly Tyr  
 49 130 135 140  
 51 Tyr Thr Met Lys Ser Asn Leu Val Met Leu Glu Asn Gly Lys Gln Leu  
 52 145 150 155 160  
 54 Thr Val Lys Arg Glu Gly Leu Tyr Tyr Val Tyr Thr Gln Val Thr Phe  
 55 165 170 175  
 57 Cys Ser Asn Arg Glu Pro Ser Ser Gln Arg Pro Phe Ile Val Gly Leu  
 58 180 185 190  
 60 Trp Leu Lys Pro Ser Ser Gly Ser Glu Arg Ile Leu Leu Lys Ala Ala  
 61 195 200 205  
 63 Asn Thr His Ser Ser Ser Gln Leu Cys Glu Gln Gln Ser Val His Leu  
 64 210 215 220  
 66 Gly Gly Val Phe Glu Leu Gln Ala Gly Ala Ser Val Phe Val Asn Val  
 67 225 230 235 240  
 69 Thr Glu Ala Ser Gln Val Ile His Arg Val Gly Phe Ser Ser Phe Gly  
 70 245 250 255  
 72 Leu Leu Lys Leu

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/842,745

DATE: 05/11/2001

TIME: 10:44:47

Input Set : A:\2922-A.txt

Output Set: N:\CRF3\05112001\I842745.raw

```

73          260
76 <210> SEQ ID NO: 2
77 <211> LENGTH: 261
78 <212> TYPE: PRT
79 <213> ORGANISM: Homo sapiens
81 <400> SEQUENCE: 2
82 Met Ile Glu Thr Tyr Asn Gln Thr Ser Pro Arg Ser Ala Ala Thr Gly
83   1          5          10          15
85 Leu Pro Ile Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu
86          20          25          30
88 Ile Thr Gln Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg
89          35          40          45
91 Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val
92          50          55          60
94 Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser
95          65          70          75          80
97 Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys
98          85          90          95
100 Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu
101          100          105          110
103 Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser
104          115          120          125
106 Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly
107          130          135          140
109 Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln
110          145          150          155          160
112 Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr
113          165          170          175
115 Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser
116          180          185          190
118 Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala
119          195          200          205
121 Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His
122          210          215          220
124 Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn
125          225          230          235          240
127 Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe
128          245          250          255
130 Gly Leu Leu Lys Leu
131          260
134 <210> SEQ ID NO: 3
135 <211> LENGTH: 33
136 <212> TYPE: PRT
137 <213> ORGANISM: PEPTIDE
139 <400> SEQUENCE: 3
140 Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile
141   1          5          10          15
143 Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu
144          20          25          30

```

Per 1.823 of Sequence Rules, the only valid <213> responses are:  
 Unknown, Artificial Sequence, or scientific name  
 (Genus/species)

(one of the three)

(see circled portion  
 of item 12 on Enov  
 summary sheet)

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/842,745

DATE: 05/11/2001  
TIME: 10:44:47

Input Set : A:\2922-A.txt  
Output Set: N:\CRF3\05112001\I842745.raw

146 Arg

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/842,745

DATE: 05/11/2001

TIME: 10:44:48

Input Set : A:\2922-A.txt

Output Set: N:\CRF3\05112001\I842745.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/842745

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
  
- 2        Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
  
- 3        Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
  
- 4        Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
  
- 5        Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
  
- 6        Variable Length      Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
  
- 7        PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s)       . Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>  
sections for Artificial or Unknown sequences.
  
- 8        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
  
- 9        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
<400> sequence id number  
000
  
- 10        Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 11        Use of "Artificial"      Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.  
(NEW RULES)      Valid response is Artificial Sequence.
  
- 12        Use of <220>Feature      Sequence(s)        are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"  
→      Please explain source of genetic material in <220> to <223> section.  
            (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
  
- 13        PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.